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Results of Comparison of Particular Domains of Hoc Proteins in *Teequatrovirinae* Subfamily Bacteriophages

Some of the more interesting results of phylogenetic analysis of particular domains in 31 proteins of *Teequatrovirinae* subfamily bacteriophages are presented. The sequences were aligned by ClustalX multiple alignment tool.

```
AR1_3 193 QATTLVVTPNSPSAGVIGTPVQFTAALASQPDGASATYKWYVDDSQIGGETNSTFNYTPT
AR1_2 97  QTTTITVTPDSPSEGVIGTAVQFTAALDSQPPGASATYQWHVDGSPVGEATDATFNYTPA
T4_2  95  QTTTLAVTPASPAAGVIGTPVQFTAALASQPDGASATYQWYVDDSQVGGETNSTFSYTPT
          *:**:.*** **: *****.******* *** ******:*:**.* :* *::**.***:
AR1_3 253 TSGVKRIKCVAQVTAENYNEKEVTSNEVSLTVNKKT
AR1_2 157 TSGVKKIKCVAQVTATDYDTKTVTSDEVSLTVNKKT
T4_2 155  TSGVKRIKCVAQVTATDYDALSVTSNEVSLTVNKKT
          *****:********* :*: ***:**********
```

Fig. 1. Multiple sequence alignment of the second and third domains of AR1 phage Hoc protein and of the second domain of T4 Hoc protein.

```
ime09_3 191 QTTTLAVTPANPAAGVIGTPVQFTAALASQPPGASATYQWYVDGSLVDGETTTTFNYTPT
ime09_2 95  QTTTLAVTPGSPDAGVIGTPIEFTAALASQPSGANATYQWHVDGSPVDEATDATFNYTPD
T4_2 95     QTTTLAVTPASPAAGVIGTPVQFTAALASQPDGASATYQWYVDDSQVGGETNSTFSYTPT
            *********..* *******::********* **.*****:**.* *. * :**.***
ime09_3 251 TVGAKTVKCVAQVTAENYNEKEVTSNEVSLTVNKKT
ime09_2 155 TSGVKKIKCVAQVTAADYDTLSVTSNEVSLTVNKKT
T4_2    155 TSGVKRIKCVAQVTATDYDALSVTSNEVSLTVNKKT
            * *.* :******** :*: .**************
```

Fig. 2. Multiple sequence alignment of the second and third domains of ime09 phage Hoc protein and of the second domain of T4 Hoc protein.

```
wV7_3 193 QATTLVVTPNSPSAGVIGTPVQFTAALASQPDGASATYKWYVDDSQIGGETNSTFNYTPT
wV7_2 97  QTTTITVTPDSPSEGVIGTAVQFTAALDSQPPGASATYQWHVDGSPVGEATDATFNYTPA
T4_2 95   QTTTLAVTPASPAAGVIGTPVQFTAALASQPDGASATYQWYVDDSQVGGETNSTFSYTPT
          *:**:.*** **: *****.******* *** ******:*:**.* :* *::**.***:
wV7_3 253 TSGVKRIKCVAQVTAENYNEKEVTSNEVSLTVNKKT
wV7_2 157 TSGVKKIKCVAQVTATDYDTKTVTSDEVSLTVNKKT
T4_2 1 55 TSGVKRIKCVAQVTATDYDALSVTSNEVSLTVNKKT
          *****:********* :*: ***:**********
```

Fig. 3. Multiple sequence alignment of the second and third domains of wV7 phage Hoc protein and of the second domain of T4 Hoc protein.

```
RB69_2 94  ENNSTVAVTPASPAAVEIGTATTFTANVSNQPSGAAIAYTWKVDGVAVDGQKQSTFEYTP
RB69_3 190 ANSSTLKITPESPTTV-FGVPITLTANVSGAPSGATTSFQWSMDDSNILDATSATYKFTP
           *.**: :** **::* :*.. *:*****. ****: :: *.:*. : . ..:*:::**
RB69_2 154 TSEGTKSITCSVTVTATDYVDKTVESSAVSLTVNKK-
RB69_3 259 TEVGSKTLKCTVSVSATNYVTKEISAEATVVTNNATF
           *. *:*::.*:*:*:**:** * :.:.*. :* * .
```

Fig. 4. Pairwise sequence alignment of the second and third domains of RB69 Hoc protein.